RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/508,759_

Source: _PCT/10_

Date Processed by STIC: _9/29/04_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
   http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , **EFS Submission User Manual - ePAVE)**
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (**EFFECTIVE 06/05/04):**
   U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/508,759

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics / Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

·2____Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

·3____Misaligned Amino Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____Variable Length Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)_____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____Skipped Sequences (OLD RULES) Sequence(s)____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) .
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

· Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences (NEW RULES) Sequence(s)_____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____Use of <220> Sequence(s)_____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

PCT

RAW SEQUENCE LISTING   DATE: 09/29/2004
PATENT APPLICATION: US/10/508,759   TIME: 16:59:56

Input Set : A:\30215APG_SEQ.txt
Output Set: N:\CRF4\09292004\J508759.raw

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     3 <110> APPLICANT: APROGEN INC.
     5 <120> TITLE OF INVENTION: HUMANIZED ANTIBODY AND PROCESS FOR PREPARING SAME
     7 <130> FILE REFERENCE: PCA30215/APG
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/508,759
C--> 9 <141> CURRENT FILING DATE: 2004-09-22
     9 <150> PRIOR APPLICATION NUMBER: KR10-2002-0015708
    10 <151> PRIOR FILING DATE: 2002-03-22
    12 <160> NUMBER OF SEQ ID NOS: 38
    14 <170> SOFTWARE: KopatentIn 1.71
    16 <210> SEQ ID NO: 1
    17 <211> LENGTH: 345
    18 <212> TYPE: DNA
    19 <213> ORGANISM: Artificial Sequence
    21 <220> FEATURE:
    22 <223> OTHER INFORMATION: HEAVY CHAIN of HZVII
    24 <400> SEQUENCE: 1
    25 caggtccagc tggtgcagtc tggagctgaa gtgaagaagc ctggggcctc agtgaaggtt    60
    27 tcctgcaaag cttctggcta caccttcacc agtgcttgga tgaactgggt gcgacaggcc   120
    29 cctggacagg gtcttgagtg gatgggacgg atttatccta gtggtggaag cactagctac   180
    31 gcacagaagt tccagggcag agtcacaatg actgcagaca atccacgag  cacagtctac   240
    33 atggagctca gcagcctgag atctgaggac acggcggtgt attactgtgc aagagagtac   300
    35 cgggttgccc gttggggcca aggaactctg gtcactgtct cttca                    345
    38 <210> SEQ ID NO: 2
    39 <211> LENGTH: 115
    40 <212> TYPE: PRT
    41 <213> ORGANISM: Artificial Sequence
    43 <220> FEATURE:
    44 <223> OTHER INFORMATION: HEAVY CHAIN of HZVII
    47 <400> SEQUENCE: 2
    48 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Ala Pro Gly Ala
    49  1               5                  10                  15
    51 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Ala
    52                 20                  25                  30
    54 Trp Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
    55             35                  40                  45
    57 Gly Arg Ile Tyr Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
    58         50                  55                  60
    60 Gln Gly Arg Val Thr Met Thr Ala Asp Lys Ser Thr Ser Thr Val Tyr
    61 65                  70                  75                  80
    63 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
    64                 85                  90                  95
    66 Ala Arg Glu Tyr Arg Val Ala Arg Trp Gly Gln Gly Thr Leu Val Thr
    67             100                 105                 110
```

give source of genetic material

Does Not Comply
Corrected Diskette Needed

see item 11 on Error Summary Sheet

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/508,759

DATE: 09/29/2004
TIME: 16:59:56

Input Set : A:\30215APG_SEQ.txt
Output Set: N:\CRF4\09292004\J508759.raw

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69 Val Ser Ala
70          115
73 <210> SEQ ID NO: 3
74 <211> LENGTH: 336
75 <212> TYPE: DNA
76 <213> ORGANISM: Artificial Sequence
78 <220> FEATURE:
79 <223> OTHER INFORMATION: LIGHT CHAIN of HZVII
82 <400> SEQUENCE: 3
83 gatatcgtga tgacccaaac tccactttct ttgtcggtta cccctggaca accagcctct      60
85 atctcttgca agtcaagtca gagcctctta tatagtaatg gaaaaaccta tttgaattgg     120
87 ttattacaga agccaggcca gcctccacag cgcctaatct atctggtgtc taatcgggac     180
89 tctggagtcc ctgacaggtt cagtggcagt ggatcaggaa cagattttac actgaaaatc     240
91 agcagagtgg aggctgagga tgttggagtt tattactgcg tgcaaggtac acattttcct     300
93 cagacgttcg gtggaggcac caaggtggaa atcaaa                               336
96 <210> SEQ ID NO: 4
97 <211> LENGTH: 112
98 <212> TYPE: PRT
99 <213> ORGANISM: Artificial Sequence
101 <220> FEATURE:
102 <223> OTHER INFORMATION: LIGHT CHAIN of HZVII
105 <400> SEQUENCE: 4
106 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
107  1               5                  10                  15
109 Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
110              20                  25                  30
112 Asn Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Lys Pro Gly Gln Pro
113          35                  40                  45
115 Pro Gln Arg Leu Ile Tyr Leu Val Ser Asn Arg Asp Ser Gly Val Pro
116      50                  55                  60
118 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
119  65                  70                  75                  80
121 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Val Gln Gly
122              85                  90                  95
124 Thr His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
125              100                 105                 110
130 <210> SEQ ID NO: 5
131 <211> LENGTH: 26
132 <212> TYPE: DNA
133 <213> ORGANISM: Artificial Sequence
135 <220> FEATURE:
136 <223> OTHER INFORMATION: Ryu94
139 <400> SEQUENCE: 5
140 gagaattcac attcacgatg tacttg                                          26
143 <210> SEQ ID NO: 6
144 <211> LENGTH: 33
145 <212> TYPE: DNA
146 <213> ORGANISM: Artificial Sequence
148 <220> FEATURE:
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149 <223> OTHER INFORMATION: HUR43-1
152 <400> SEQUENCE: 6
153 ctgctgcagc tggacctgac tctggacacc att                          33
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157 <211> LENGTH: 33
158 <212> TYPE: DNA
159 <213> ORGANISM: Artificial Sequence
161 <220> FEATURE:
162 <223> OTHER INFORMATION: HUR44-1
165 <400> SEQUENCE: 7
166 caggtccagc tgcagcagtc tggacctgaa ctg                          33
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171 <212> TYPE: DNA
172 <213> ORGANISM: Artificial Sequence
174 <220> FEATURE:
175 <223> OTHER INFORMATION: HUR45-1
178 <400> SEQUENCE: 8
179 tgggcccttg gtggaggctg cagagacagt gac                          33
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183 <211> LENGTH: 33
184 <212> TYPE: DNA
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: HUR46-1
191 <400> SEQUENCE: 9
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196 <211> LENGTH: 28
197 <212> TYPE: DNA
198 <213> ORGANISM: Artificial Sequence
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201 <223> OTHER INFORMATION: HUR31
204 <400> SEQUENCE: 10
205 cagcggccgc tcatttaccc ggggacag                               28
208 <210> SEQ ID NO: 11
209 <211> LENGTH: 26
210 <212> TYPE: DNA
211 <213> ORGANISM: Artificial Sequence
213 <220> FEATURE:
214 <223> OTHER INFORMATION: Ryu86
217 <400> SEQUENCE: 11
218 caaagcttgg aagcaagatg gattca                                 26
221 <210> SEQ ID NO: 12
222 <211> LENGTH: 27
223 <212> TYPE: DNA
224 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
227 <223> OTHER INFORMATION: HUR48
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234 <210> SEQ ID NO: 13
235 <211> LENGTH: 27
236 <212> TYPE: DNA
237 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
240 <223> OTHER INFORMATION: HUR49
243 <400> SEQUENCE: 13
244 tgtggggata tcttgatgac ccaaact                                      27
247 <210> SEQ ID NO: 14
248 <211> LENGTH: 27
249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
253 <223> OTHER INFORMATION: HUR50
256 <400> SEQUENCE: 14
257 cacagatctt ttgatttcca gcttggt                                      27
260 <210> SEQ ID NO: 15
261 <211> LENGTH: 27
262 <212> TYPE: DNA
263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
266 <223> OTHER INFORMATION: HUR51
269 <400> SEQUENCE: 15
270 atcaaaagat ctgtggctgc accatct                                      27
273 <210> SEQ ID NO: 16
274 <211> LENGTH: 58
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence
278 <220> FEATURE:
279 <223> OTHER INFORMATION: CK1D
282 <400> SEQUENCE: 16
283 gcgccgtcta gaattaacac tctcccctgt tgaagctctt tgtgacgggc gaactcag     58
286 <210> SEQ ID NO: 17
287 <211> LENGTH: 27
288 <212> TYPE: DNA
289 <213> ORGANISM: Artificial Sequence
291 <220> FEATURE:
292 <223> OTHER INFORMATION: YM001N
295 <400> SEQUENCE: 17
296 ccggaattca cattcacgat gtacttg                                      27
299 <210> SEQ ID NO: 18
300 <211> LENGTH: 16
301 <212> TYPE: DNA
302 <213> ORGANISM: Artificial Sequence
304 <220> FEATURE:
305 <223> OTHER INFORMATION: YM003
308 <400> SEQUENCE: 18
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312 <210> SEQ ID NO: 19
313 <211> LENGTH: 33
314 <212> TYPE: DNA
315 <213> ORGANISM: Artificial Sequence
317 <220> FEATURE:
318 <223> OTHER INFORMATION( ym257 )
321 <400> SEQUENCE: 19
322 acgcattcag tgcttcttgg atgaactggg tga                         33
325 <210> SEQ ID NO: 20
326 <211> LENGTH: 31
327 <212> TYPE: DNA
328 <213> ORGANISM: Artificial Sequence
330 <220> FEATURE:
331 <223> OTHER INFORMATION( YM258 )
334 <400> SEQUENCE: 20
335 atccaagaag cactgaatgc gtagccagaa g                           31
338 <210> SEQ ID NO: 21
339 <211> LENGTH: 38
340 <212> TYPE: DNA
341 <213> ORGANISM: Artificial Sequence
343 <220> FEATURE:
344 <223> OTHER INFORMATION:( YM004 )
347 <400> SEQUENCE: 21
348 ccaattcaaa gcggtttttc cattactata taagaggc                    38
351 <210> SEQ ID NO: 22
352 <211> LENGTH: 32
353 <212> TYPE: DNA
354 <213> ORGANISM: Artificial Sequence
356 <220> FEATURE:
357 <223> OTHER INFORMATION( YM009 )
360 <400> SEQUENCE: 22
361 gcagccaccg tacgtttgat ttccaccttg gt                          32
364 <210> SEQ ID NO: 23
365 <211> LENGTH: 39
366 <212> TYPE: DNA
367 <213> ORGANISM: Artificial Sequence
369 <220> FEATURE:
370 <223> OTHER INFORMATION: Ryu 166 )
373 <400> SEQUENCE: 23
374 ggatttgtct gcagtcattg tggctctgcc ctggaactt                   39
377 <210> SEQ ID NO: 24
378 <211> LENGTH: 27
379 <212> TYPE: DNA
380 <213> ORGANISM: Artificial Sequence
382 <220> FEATURE:
383 <223> OTHER INFORMATION: Hur 37 )
386 <400> SEQUENCE: 24
387 gacaaatcca cgagcacagt ctacatg                                27
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Please correct this type of error in subsequent sequences.

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/508,759

DATE: 09/29/2004
TIME: 16:59:57

Input Set : **A:\30215APG_SEQ.txt**
Output Set: **N:\CRF4\09292004\J508759.raw**

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date